Aslam alikum

Today we will respond to the number one evidence for evolution and the most common icon in evolution theory

The genetic similarity between humans and chimpanzees

Now this argument is based on the similarity of the genetic information (DNA)

between two species as evidence for common descent after they failed in proving that from paleontology field because it's just speculations and cherry-picking for data

But the problem with that evidence is that it's not like what people think !!

When you hear the statement we share %98 Of our DNA with chimpanzees

You will think that he is talking about all the genetic informations you have like comparing all the genetic informations between us and came to this conclusion

But is that really the case ?

The answer is simply NO !!!

what scientists did was a process of selection and cherry picking of data again by using a software to come to such a conclusion

In order to reach this point %98 they need to eliminate all the non coding DNA like《introns *DNA sequence of the F traALE region that includes the gene for F pilin* and large amounts from the CDNA》

Which means that they only took 1.9 million nitrogen bases and compared them to 3 billion nitrogen bases

Additional article information

## Abstract

A total of 8,859 DNA sequences encompassing ~1.9 million base pairs of the chimpanzee genome were sequenced and compared to corresponding human DNA sequences. Although the average sequence difference is low (1.24%), the extent of changes is markedly different among sites and types of substitutions. Whereas ~15% of all CpG sites have experienced changes between humans and chimpanzees, owing to a 23-fold excess of transitions and a 7-fold excess of transversions, substitutions at other sites vary in frequency, between 0.1% and 0.5%. If the nucleotide diversity in the common ancestral species of humans and chimpanzees is assumed to hav



## Discussion

### Substitution Patterns

The comparison between 1.9 Mb of genomic DNA derived from >8,000 individual DNA sequences of the chimpanzee genome and the corresponding DNA sequences in the human genome reveals a mean sequence difference of 1.24%. This is in agreement with a recent study (Chen and Li 2001) in which the same sequence difference was seen when a total of 24 kb from 53 autosomal regions were compared.

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC379137/

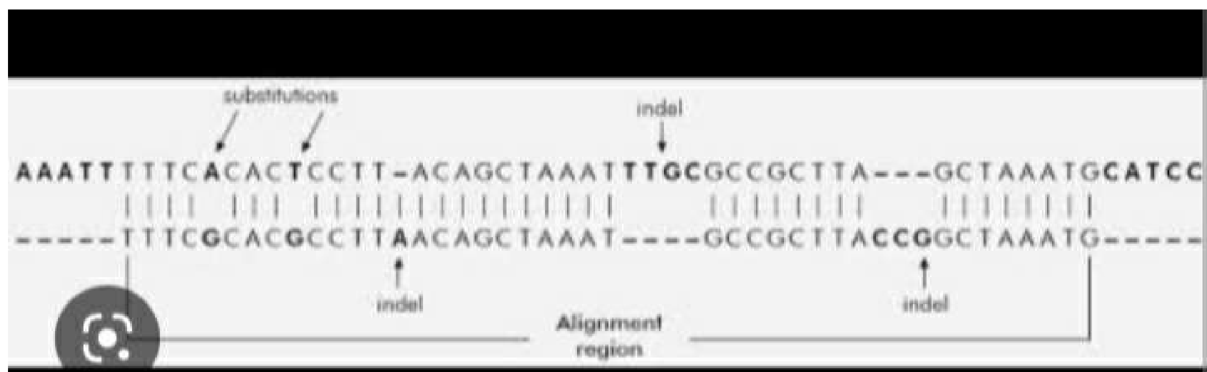
So imagine the number of the nitrogen bases that will be eliminated by the software in order to get the %98 similarity They only compared %0.064 of our genomes

So imagine the number of the nitrogen bases that will be eliminated by the software in order to get the %98 similarity They only compared %0.064 of our genomes And the reason why did that is that they thought that the non cDNA has no function so they assumed it has no importance to compare and went to the coding DNA directly but this assumption has many problems
1) the non cDNA do have essential functions that's why new scientific papers calling it the hiding treasure

2) the assumption that similarity of the coding DNA is evidence for common dissent is not necessarily true it's an assumption only based on logical fallacie For example

when I look at different types of cars I will find that there is something common between them for example all the cars has wheels but I will assume that since all cars has wheels therefore only one company made all these different types of cars why because all of them has wheels but what will you tell me is no they have wheels because wheels are essential for movement so they had this similarity in order to serve certain function so companies shared the same structure to serve the same purpose this is exactly the same thing regarding the coding DNA when you have genes responsible for producing proteins and this proteins has certain function so they should have certain similarity because they have similar function like for example the (HB) gene it has the same exact function between other animals because it is responsible to produce the protein hemoglobin which is helping in carrying the oxygen and carbon dioxide so because we had similar functions in our bodies it is normal thing to find certain similarity in our genes because the designer our creator made this gene similar to certain level to serve the same function so that's why the Assumption of saying that genetic similarity is a direct evidence for common descent is not logical argument at all

and after we clarified this counter argument
We will go to the gene bank to show you guys how did they do this comparison process




But first let's look at how does the the software works so it will be easier to understand

So as you see the software will count only what called the substitutions as differences wich is having for example the code (A) in human side and (G) in the chimpanzee side only one code isolated code will be counted but if I found any group difference like (AAATT) in human and not in chimpanzees it will be eliminated just like that And to understand the full picture we are going now to the gene bank

We take gene for example the HB gene which according to the evolutionists it's 100% identical!!

http://www.ensembl.org/Pan_troglodytes/Gene/Sequence?g=ENSPTRG00000040047;r=11:4980274-4982001;t=ENSPTRT00000006177

Ensembl BLAST/BLAT | VEP

Chimpanzee (Pan_tro_3.0)

Gene: HBB

Marked up sequence

[redacted]

>chromosome:Fun_tru.3.0:11:4977674:4982601:-1
GGTCTCTAGTTTTTTATCTCTTGTTTCCCAAAACCTAATAAGTAACTAATGCACAGAGCA
CATTGATTTGTATTTATTCTATTTTTAGACATAATTTATTAGCATGCATGAGCAAATTAA
GAAAAACAACAACAAATGAATGCATATATATGTATATGTATGTGTGTAAATATACATATA
TATATATATATATATATTTCTTTTCTTACCAGAAGTTTTTAATCCAAATCAGGAGAAGAT
ATGCTTAGAACTGAGGTAGAGTTTTCATCCATTCTGTCCTGTAAGTATTTTGCATATTCT
GGAGACACAGGAAGAGATCCATCTACACATCCCAAAGCTGAATTATGGTAGACAAAACTC
TTCCACTTTTAGTGGATGAATTTCTTATTTGTGTAATAAGAAAATTGGGAAAACGGATCTT
CAATATGCTTACCAAGCTGTGATTCCAAATATTACGTAAACACACTTGCAAAGGAGGATG
TTTTTAGTAGCAATTTGTACTGATGGTGTGGGGCCAAGAGATATATCTTAGAGGGAGGGC
TGAGGGTTTGAAGTCCAACTCCTAAGCCAGTGCCAGAAGAGCCAAGGACAGGTATGGGTG
TCATCACTTAGACCTCACCCTGTGGAGCCACACCCTAGGGTTGGCCAATCTACTCCCAGG
AGCAGGGAGGGCAGGAGCCAGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTT
ACATTTGCTTCTGACACAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACG
TGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAG
TTGGTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTTACAAGACAGGCTTAAGGAGACCA
GTAGAAACTGGGCATGTGGAGACAGAGAACACTCTTGGGTTTCTGATAGGCACTGACTCT
CTCTGCCTATTGGGCTATTTTCCCACCCTTAGGCTGCTGGTGGTCTACCCTTGGACCCAG
AGGTTCTTTGAGTCCTTTGGGGATCTGTCCACTCCTGATGCTGTTATGGGCAACCCTAAG
GTGAAGGCTCATGGCAAGAAAGTGCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGAC
AACCTCAAGGGCACCTTTGCCACACTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGAT
CCTGAGAACTTCAGGGTGAGTCTATGGGACCCTTGATGTTTTCTTTCCCCTTCTTTTCTA
TGGTTAAGTTCATGTCATAGGAAGGGGATAAGTAACAGGGTACAGTTTAGAATGGGAAAC
AGACGAATGATTGCATCAGTGTGGAACTCTCAGGATCATTTTAGTTTCTTTTATTTGCTG
TTCATAACAATTGTTTTCTTTTGTTTAATTCTTGGTTTCTTTTTTTTTCTTCTCTGCAAT
TTTTACTATTATACTTAATGCCTTAACGTTGTGTATAACAAAAGGAAATATCTCTGAGAT
ACATTAAGTAACTTAAAAAAAATGTTTACGCAGTCTGCTAGTACATTACTATTTGGAAT
ATATGTGTGCTTATTTGCATATTCATAATGTACCTACTTTATTTTCTTTTATTTTTAATT
GATACATAATCATTATACATATTTATGGGTTAAAGTGTAATGTTTTAATATGTGTACACA
TATTGACCAAATCAGGGTAATTTTGCATTTGTTATTTTAAAAAATGCTTTCTTCTTTTAA
TATACTTTTTGTTTATCTTATTTCTACTACTTTCCCTAATCTCTTTCTTTCAGGGCAAT
AATGATACAATGTATCATGCCTCTTTGCACCATTCTAAAGAATAACAGTGATAATTTGTG
GGTTAAGGCAATAGCAATATTTCTGCATATAAATATTTCTGCATATAAATTGTAACTGAT
GTAAGAGGTTTCATATTGCTAATAGCAGCTACAATCCAGCTACCATTCTTCTTTTATTTT
ATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTAGGCCCTTTTGCTAATCATGTT
CATACCTCTTGTCTTCCTGGCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCA
TCACTTTGGCAAAGAATTCACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGG
TGTGGCTAATGCCCTGGCCCACAAGTATCACTAAGCTCGCTTTCTTGCTGTCCAATTTCT
ATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTACTAAACTGGGGGATATTATGAAGGGCC
TTGAGCATCTGGATTCTGCCTAATAAAAAACATTTATTTTCATTGCAATGGTGTATTTAA
ATTATTTCTGAATATTTTACTAAAAAGGGAATGTGGGAGGTCAGTGCATTTAAAACATAA
AGAAATGAAGAGCTAGTTCAAACCTTGGGAAAATACACTATATCTTAAACTCCATGAAAG
AAGGTGAGGCTGCAAACAGCTAATGCACATTGGCAACAGCCCCTGATGCCTATGCCTTAT
TCATCCCTCAGAAAAGGATTCAAGTAGAGGCTTGATTTGGAGGTTAAAGTTTTGCTATGC
TGTATTTTACATTACTTATTGTTTTAGCTGTCCTCATGAATGTCTTTTCACTATGCATTT
GCTTATCCTGCATCTCTCAGCCTTGACTCCACTGAGTTCTCTTGCTTAGAGATACTAGCT
TTCCCCTAAAGTGCTCCTTCCATGTTTTACGGGGAGATGGTTTCTCCTCCCTGGCCACT
CAGTCTTAGTTGTCTCTGTTGTCTTATAGAGGTCTACTTGAAGAAGGAAAAACAGGGTC
ATGGTTTGACTGTCCTGTGAGCCCTTCTTCCCTGCCTGCCCCACTCACAGTGACCCAGAA
TCTGCAGTGCTAGTCTCCGGGAACTTTCACTCTTTCACAGTCTGCTTT

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[redacted]

[redacted]

ensembl.org/Pan_troç

00000040047

hemoglobin subunit beta [Source:VGNC Symbol;Acc:VGNC:3255]

Chromosome 11: 4,980,274-4,982,001 reverse strand.

Pan_tro_3.0:CM000325.3

This gene has 1 transcript (splice variant), 525 orthologues and 13 paralogues.

Hide transcript table

idden)

| Name | bp | Protein | Biotype | UniProt Matc |
|---|---|---|---|---|
| HBB-201 | 748 | 147aa | Protein coding | A0A2J8P6S4 A0A663D |

ıce

BLAST this sequence

exons All exons in this region

ed

```
3.0:11:4979674:4982601:-1
TTGTTTGCCCAAAACCTAATAAGTAACTAATGCACAGAGCA
ATTTTTAGACATAATTTATTAGCATGCATGAGCAAATTAA
TGCATATATATATGTATATATGTATGTGTGTAAATATACATATA
TTTTCTTACCAGAAGGTTTTAATCCAAATCAGGAGAAGAT
GTTTTCATCCATTCTGTCCTGTAAGTATTTTGCATATTCT
ATCTACACATCCCAAAGCTGAATTATGGTAGACAAAACTC
```

[redacted]

This is the chimpanzees HB gene on the gene bank

http://www.ensembl.org/Homo_sapiens/Gene/Sequence?g=ENSG00000244734;r=11:5225464-5229395

Ensembl

Marked up sequence

[redacted]

[illegible]



[redacted]

ensembl.org/Homo_s

More ▾ Search Human...

000244734

hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:4827]

CD113t-C, beta-globin

Chromosome 11: 5,225,464-5,229,395 reverse strand.

GRCh38:CM000673.2

This gene has 6 transcripts (splice variants), 525 orthologues, 11 paralogues and is associated with 28 phenotypes.

Hide transcript table

hidden)

| ame | bp | Protein | Biotype | CCDS | UniProt Match |
|---|---|---|---|---|---|
| B-201 | 628 | 147aa | Protein coding | CCDS7753 | D9YZU5 P68871 |
| B-202 | 502 | 90aa | Protein coding | | F8W6P5 |
| B-203 | 319 | No protein | Retained intron | | - |
| B-204 | 680 | 111aa | Protein coding | | A0A2R8Y7R2 |
| B-205 | 609 | 55aa | Nonsense mediated decay | | A0A0J9YWK4 |
| B-206 | 754 | 147aa | Protein coding | CCDS7753 | D9YZU5 P68871 |

nce

BLAST this sequence

3 exons All exons in this region

ded

And this is the human HB gene on gene bank 👆

Okay so what can you see is orange Line which called the exons and you have also the white lines which called the introns and what can you see is that there is many differences between these two genes like for example you can see the different positions of the Orange Lines and and the white one the intron and exons you can see the different length of each one and you can see even the different structure of the gene in total and also there's something called the splicing variant the humans have six of them chimpanzees has only one

There function is mostly producing different types of proteins in humans 5 of them producing different types of proteins
In chimpanzees only one producing one protein
But stell for them it 100% identical

Let's go deeper to understand the point view of the scientists
http://www.ensembl.org/Homo_sapiens/Transcript/Sequence_cDNA?db=core;g=ENSG00000244734;r=11:5225464-5229395;t=ENST00000335295



[redacted]

Missense Protein altering variant Splice region Start lost Stop gained

Synonymous

Other UTR

Markup loaded

• Variants are filtered by consequence type

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[redacted]

This is only the coding part of the HB gene in humans

http://www.ensembl.org/Pan_troglodytes/Transcript/Sequence_cDNA?db=core;g=ENSPTRG00000040047;r=11:4980274-4982001;t=ENSPTRT00000006177

[redacted]

Ensembl

Chimpanzee (Pan_tro_3.0)

Transcript: ENSPTRT00000006177.4

cDNA sequence

[redacted]

And this one is the coding part of the HB gene for chimpanzees👆

Now what you can can see is group of lines each group is made of three lines the first and the second is the nitrogen bases and the third is for the amino acids responsible to produce
What we will need is only the the middle line of codes which started with ATGGTGCA Which bee contend in the counting process This part is the only part that gives 100% similarity Only 444 codes out of 50,000 one from the humans that has been counted the others has been eliminated

So next time when someone tells you this selly argument you know what is the answer insha ALLAH

Wa aslam alikum